



H3

SEQUENCE LISTING

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<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY5,
EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES

<130> DOO41NP

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 Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys
 35 40 45
 Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly
 50 55 60
 Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala
 65 70 75 80
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Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln
85 90 95

Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu
100 105 110

Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys
115 120 125

Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr
130 135 140

Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser
145 150 155 160

Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu Asn
165 170 175

His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu His
180 185 190

Gln Leu Thr Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile Ser
195 200 205

Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met Val
210 215 220

Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met Pro
225 230 235 240

Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu Thr
245 250 255

Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Phe Leu Pro
260 265 270

Arg Asn Gln Ile Gly Phe Val Pro Glu Lys Thr Phe Ser Ser Leu Lys
275 280 285

Asn Leu Gly Glu Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser
290 295 300

Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asn Leu Ser
305 310 315 320

Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln Phe Glu Ser Leu Lys
325 330 335

Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile Asn
340 345 350

Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe Lys
355 360 365

Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val Arg Ile Cys Met Pro
370 375 380

Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn Ile
385 390 395 400

Leu Arg Ile Phe Val Trp Val Ile Ala Phe Ile Thr Cys Phe Gly Asn
405 410 415

Leu Phe Val Ile Gly Met Arg Ser Phe Ile Lys Ala Glu Asn Thr Thr
420 425 430

His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala Asp Cys Leu Met Gly
435 440 445

Val Tyr Leu Phe Phe Val Gly Ile Phe Asp Ile Lys Tyr Arg Gly Gln
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Tyr Gln Lys Tyr Ala Leu Leu Trp Met Glu Ser Val Gln Cys Arg Leu
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Met Gly Phe Leu Ala Met Leu Ser Thr Glu Val Ser Val Leu Leu Leu
485 490 495

Thr Tyr Leu Thr Leu Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser
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Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile Cys Ile
515 520 525

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530 535 540

Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu Tyr
545 550 555 560

Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser Leu Gly Ile
565 570 575

Phe Leu Gly Val Asn Leu Leu Ala Phe Leu Ile Ile Val Phe Ser Tyr
580 585 590

Ile Thr Met Phe Cys Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr Glu
595 600 605

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610 615 620

Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val Val
625 630 635 640

Lys Ile Leu Ser Leu Phe Arg Val Glu Ile Pro Asp Thr Met Thr Ser
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Trp Ile Val Ile Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro Ile
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Leu Tyr Thr Leu Thr Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln Leu
675 680 685

Leu His Lys His Gln Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys Ser
690 695 700

Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser Ser Ser Leu Lys Leu
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Gly Val Leu Asn Lys Ile Thr Leu Gly Asp Ser Ile Met Lys Pro Val
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Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys
35 40 45

Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly
50 55 60

Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala
65 70 75 80

Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln
85 90 95

Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu
100 105 110

Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys
115 120 125

Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr
130 135 140

Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser
145 150 155 160

Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Ile Leu Asp
165 170 175

Asp Asn Pro Ile Thr Arg Ile Ser Gln Arg Leu Phe Thr Gly Leu Asn
180 185 190

Ser Leu Phe Phe Leu Ser Met Val Asn Asn Tyr Leu Glu Ala Leu Pro
195 200 205

Lys Gln Met Cys Ala Gln Met Pro Gln Leu Asn Trp Val Asp Leu Glu
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Gly Asn Arg Ile Lys Tyr Leu Thr Asn Ser Thr Phe Leu Ser Cys Asp
225 230 235 240

Ser Leu Thr Val Leu Phe Leu Pro Arg Asn Gln Ile Gly Phe Val Pro
245 250 255

Glu Lys Thr Phe Ser Ser Leu Lys Asn Leu Gly Glu Leu Asp Leu Ser
260 265 270

Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu Phe Lys Asp Leu Lys
275 280 285

Leu Leu Gln Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr Leu His
290 295 300

Lys Asn Gln Phe Glu Ser Leu Lys Gln Leu Gln Ser Leu Asp Leu Glu
305 310 315 320

Arg Ile Glu Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met Lys
325 330 335

Asn Leu Ser His Ile Tyr Phe Lys Asn Phe Arg Tyr Cys Ser Tyr Ala
340 345 350

Pro His Val Arg Ile Cys Met Pro Leu Thr Asp Gly Ile Ser Ser Phe
355 360 365

Glu Asp Leu Leu Ala Asn Asn Ile Leu Arg Ile Phe Val Trp Val Ile
370 375 380

Ala Phe Ile Thr Cys Phe Gly Asn Leu Phe Val Ile Gly Met Arg Ser
385 390 395 400

Phe	Ile	Lys	Ala	Glu	Asn	Thr	Thr	His	Ala	Met	Ser	Ile	Lys	Ile	Leu
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Cys	Cys	Ala	Asp	Cys	Leu	Met	Gly	Val	Tyr	Leu	Phe	Phe	Val	Gly	Ile
						420			425						430
Phe	Asp	Ile	Lys	Tyr	Arg	Gly	Gln	Tyr	Gln	Lys	Tyr	Ala	Leu	Leu	Trp
						435			440						445
Met	Glu	Ser	Val	Gln	Cys	Arg	Leu	Met	Gly	Phe	Leu	Ala	Met	Leu	Ser
						450			455						460
Thr	Glu	Val	Ser	Val	Leu	Leu	Leu	Thr	Tyr	Leu	Thr	Leu	Glu	Lys	Phe
						465			470						480
Leu	Val	Ile	Val	Phe	Pro	Phe	Ser	Asn	Ile	Arg	Pro	Gly	Lys	Arg	Gln
						485			490						495
Thr	Ser	Val	Ile	Leu	Ile	Cys	Ile	Trp	Met	Ala	Gly	Phe	Leu	Ile	Ala
						500			505						510
Val	Ile	Pro	Phe	Trp	Asn	Lys	Asp	Tyr	Phe	Gly	Asn	Phe	Tyr	Gly	Lys
						515			520						525
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						530			535						540
Ser	Lys	Gly	Tyr	Ser	Leu	Gly	Ile	Phe	Leu	Gly	Val	Asn	Leu	Leu	Ala
						545			550						560
Phe	Leu	Ile	Ile	Val	Phe	Ser	Tyr	Ile	Thr	Met	Phe	Cys	Ser	Ile	Gln
						565			570						575
Lys	Thr	Ala	Leu	Gln	Thr	Thr	Glu	Val	Arg	Asn	Cys	Phe	Gly	Arg	Glu
						580			585						590
Val	Ala	Val	Ala	Asn	Arg	Phe	Phe	Ile	Val	Phe	Ser	Asp	Ala	Ile	
						595			600						605
Cys	Trp	Ile	Pro	Val	Phe	Val	Val	Lys	Ile	Leu	Ser	Leu	Phe	Arg	Val
						610			615						620
Glu	Ile	Pro	Asp	Thr	Met	Thr	Ser	Trp	Ile	Val	Ile	Phe	Phe	Leu	Pro
						625			630						640
Val	Asn	Ser	Ala	Leu	Asn	Pro	Ile	Leu	Tyr	Thr	Leu	Thr	Thr	Asn	Phe
						645			650						655

Phe Lys Asp Lys Leu Lys Gln Leu Leu His Lys His Gln Arg Lys Ser
660 665 670

Ile Phe Lys Ile Lys Lys Ser Leu Ser Thr Ser Ile Val Trp Ile
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Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu Asn Lys Ile Thr Leu
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Gly Asp Ser Ile Met Lys Pro Val Ser
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HGPRBMY4 5'
primer

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<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
oligos

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<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
oligos

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Ser Pro Pro Thr Leu Cys Ser Val Glu Gly Thr Phe His Cys Asp Asp
 35 40 45

Gly Met Leu Gln Cys Val Leu Met Gly Ser Lys Cys Asp Gly Val Ser
 50 55 60

Asp Cys Glu Asn Gly Met Asp Glu Ser Val Glu Thr Cys Gly Cys Leu
 65 70 75 80

Gln Ser Glu Phe Gln Cys Asn His Thr Thr Cys Ile Asp Lys Ile Leu
 85 90 95

Arg Cys Asp Arg Asn Asp Asp Cys Ser Asn Gly Leu Asp Glu Arg Glu
 100 105 110

Cys Asp Ile Tyr Ile Cys Pro Leu Gly Thr His Val Lys Trp His Asn
 115 120 125

His Phe Cys Val Pro Arg Asp Lys Gln Cys Asp Phe Leu Asp Asp Cys
 130 135 140

Gly Asp Asn Ser Asp Glu Lys Ile Cys Glu Arg Arg Glu Cys Val Ala
 145 150 155 160

Thr Glu Phe Lys Cys Asn Asn Ser Gln Cys Val Ala Phe Gly Asn Leu
 165 170 175

Cys Asp Gly Leu Val Asp Cys Val Asp Gly Ser Asp Glu Asp Gln Val
 180 185 190

Ala Cys Asp Ser Asp Lys Tyr Phe Gln Cys Ala Glu Gly Ser Leu Ile

195

200

205

Lys Lys Glu Phe Val Cys Asp Gly Trp Val Asp Cys Lys Leu Thr Phe
 210 215 220

Ala Asp Glu Leu Asn Cys Lys Leu Cys Asp Glu Asp Asp Phe Arg Cys
 225 230 235 240

Ser Asp Thr Arg Cys Ile Gln Lys Ser Asn Val Cys Asp Gly Tyr Cys
 245 250 255

Asp Cys Lys Thr Cys Asp Asp Glu Glu Val Cys Ala Asn Asn Thr Tyr
 260 265 270

Gly Cys Pro Met Asp Thr Lys Tyr Met Cys Arg Ser Ile Tyr Gly Glu
 275 280 285

Pro Arg Cys Ile Asp Lys Asp Asn Val Cys Asn Met Ile Asn Asp Cys
 290 295 300

Arg Asp Gly Asn Val Gly Thr Asp Glu Tyr Tyr Cys Ser Asn Asp Ser
 305 310 315 320

Glu Cys Lys Asn Phe Gln Ala Ala Met Gly Phe Phe Tyr Cys Pro Glu
 325 330 335

Glu Arg Cys Leu Ala Lys His Leu Tyr Cys Asp Leu His Pro Asp Cys
 340 345 350

Ile Asn Gly Glu Asp Glu Gln Ser Cys Leu Ala Pro Pro Lys Cys Ser
 355 360 365

Gln Asp Glu Phe Gln Cys His His Gly Lys Cys Ile Pro Ile Ser Lys
 370 375 380

Arg Cys Asp Ser Val His Asp Cys Val Asp Trp Ser Asp Glu Met Asn
 385 390 395 400

Cys Glu Asn His Gln Cys Ala Ala Asn Met Lys Ser Cys Leu Ser Gly
 405 410 415

His Cys Ile Glu Glu His Lys Trp Cys Asn Phe His Arg Glu Cys Pro
 420 425 430

Asp Gly Ser Asp Glu Lys Asp Cys Asp Pro Arg Pro Val Cys Glu Ala
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Asn Gln Phe Arg Cys Lys Asn Gly Gln Cys Ile Asp Pro Leu Gln Val

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465	470	475
Ile Asn Cys Ser Gln His Ile Cys Leu Glu Gly Gln Phe Arg Cys Arg		
485	490	495
Lys Ser Phe Cys Ile Asn Gln Thr Lys Val Cys Asp Gly Thr Val Asp		
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Cys Leu Gln Gly Met Trp Asp Glu Asn Asn Cys Arg Tyr Trp Cys Pro		
515	520	525
His Gly Gln Ala Ile Cys Gln Cys Glu Gly Val Thr Met Asp Cys Thr		
530	535	540
Gly Gln Lys Leu Lys Glu Met Pro Val Gln Gln Met Glu Glu Asp Leu		
545	550	555
Ser Lys Leu Met Ile Gly Asp Asn Leu Leu Asn Leu Thr Ser Thr Thr		
565	570	575
Phe Ser Ala Thr Tyr Tyr Asp Lys Val Thr Tyr Leu Asp Leu Ser Arg		
580	585	590
Asn His Leu Thr Glu Ile Pro Ile Tyr Ser Phe Gln Asn Met Trp Lys		
595	600	605
Leu Thr His Leu Asn Leu Ala Asp Asn Asn Ile Thr Ser Leu Lys Asn		
610	615	620
Gly Ser Leu Leu Gly Leu Ser Asn Leu Lys Gln Leu His Ile Asn Gly		
625	630	635
Asn Lys Ile Glu Thr Ile Glu Glu Asp Thr Phe Ser Ser Met Ile His		
645	650	655
Leu Thr Val Leu Asp Leu Ser Asn Gln Arg Leu Thr His Val Tyr Lys		
660	665	670
Asn Met Phe Lys Gly Leu Lys Gln Ile Thr Val Leu Asn Ile Ser Arg		
675	680	685
Asn Gln Ile Asn Ser Ile Asp Asn Gly Ala Phe Asn Asn Leu Ala Asn		
690	695	700
Val Arg Leu Ile Asp Leu Ser Gly Asn Val Ile Lys Asp Ile Gly Gln		

705	710	715	720
Lys Val Phe Met Gly Leu Pro Arg Leu Val Glu Leu Lys Thr Asp Ser			
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Tyr Arg Phe Cys Cys Leu Ala Pro Glu Gly Val Lys Cys Ser Pro Lys			
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Gln Asp Glu Phe Ser Ser Cys Glu Asp Leu Met Ser Asn His Val Leu			
755	760	765	
Arg Val Ser Ile Trp Val Leu Gly Val Ile Ala Leu Val Gly Asn Phe			
770	775	780	
Val Val Ile Phe Trp Arg Val Arg Asp Phe Arg Gly Gly Lys Val His			
785	790	795	800
Ser Phe Leu Ile Thr Asn Leu Ala Ile Gly Asp Phe Leu Met Gly Val			
805	810	815	
Tyr Leu Leu Ile Ile Ala Thr Ala Asp Thr Tyr Tyr Arg Gly Val Tyr			
820	825	830	
Ile Ser His Asp Glu Asn Trp Lys Gln Ser Gly Leu Cys Gln Phe Ala			
835	840	845	
Gly Phe Val Ser Thr Phe Ser Ser Glu Leu Ser Val Leu Thr Leu Ser			
850	855	860	
Thr Ile Thr Leu Asp Arg Leu Ile Cys Ile Leu Phe Pro Leu Arg Arg			
865	870	875	880
Thr Arg Leu Gly Leu Arg Gln Ala Ile Ile Val Met Ser Cys Ile Trp			
885	890	895	
Val Leu Val Phe Leu Leu Ala Val Leu Pro Leu Leu Gly Phe Ser Tyr			
900	905	910	
Phe Glu Asn Phe Tyr Gly Arg Ser Gly Val Cys Leu Ala Leu His Val			
915	920	925	
Thr Pro Asp Arg Arg Pro Gly Trp Glu Tyr Ser Val Gly Val Phe Ile			
930	935	940	
Leu Leu Asn Leu Leu Ser Phe Val Leu Ile Ala Ser Ser Tyr Leu Trp			
945	950	955	960
Met Phe Ser Val Ala Lys Lys Thr Arg Ser Ala Val Arg Thr Ala Glu			

965

970

975

Ser Lys Asn Asp Asn Ala Met Ala Arg Arg Met Thr Leu Ile Val Met
 980 985 990

Thr Asp Phe Cys Cys Trp Val Pro Ile Ile Val Leu Gly Phe Val Ser
 995 1000 1005

Leu Ala Gly Ala Arg Ala Asp Asp Gln Val Tyr Ala Trp Ile Ala Val
 1010 1015 1020

Phe Val Leu Pro Leu Asn Ser Ala Thr Asn Pro Val Ile Tyr Thr Leu
 1025 1030 1035 1040

Ser Thr Ala Pro Phe Leu Gly Asn Val Arg Lys Arg Ala Asn Arg Phe
 1045 1050 1055

Arg Lys Ser Phe Ile His Ser Phe Thr Gly Asp Thr Lys His Ser Tyr
 1060 1065 1070

Val Asp Asp Gly Thr Thr His Ser Tyr Cys Glu Lys Lys Ser Pro Tyr
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Arg Gln Leu Glu Leu Lys Arg Leu Arg Ser Leu Asn Ser Ser Pro Pro
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Met Tyr Tyr Asn Thr Glu Leu His Ser Asp Ser
 1105 1110 1115

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 <213> RAT

<400> 11
 Met Ala Leu Leu Leu Val Ser Leu Leu Ala Phe Leu Gly Thr Gly Ser
 1 5 10 15

Gly Cys His His Trp Leu Cys His Cys Ser Asn Arg Val Phe Leu Cys
 20 25 30

Gln Asp Ser Lys Val Thr Glu Ile Pro Thr Asp Leu Pro Arg Asn Ala
 35 40 45

Ile Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Pro Lys Gly
 50 55 60

Ser Phe Ala Gly Phe Gly Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn
65 70 75 80

Asp Val Leu Glu Val Ile Glu Ala Asp Val Phe Ser Asn Leu Pro Lys
85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asn
100 105 110

Pro Glu Ala Phe Gln Asn Leu Pro Ser Leu Arg Tyr Leu Leu Ile Ser
115 120 125

Asn Thr Gly Ile Lys His Leu Pro Ala Val His Lys Ile Gln Ser Leu
130 135 140

Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Ile Val
145 150 155 160

Ala Arg Asn Ser Phe Met Gly Leu Ser Phe Glu Ser Val Ile Leu Trp
165 170 175

Leu Ser Lys Asn Gly Ile Glu Glu Ile His Asn Cys Ala Phe Asn Gly
180 185 190

Thr Gln Leu Asp Glu Leu Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu
195 200 205

Leu Pro Asn Asp Val Phe Gln Gly Ala Ser Gly Pro Val Ile Leu Asp
210 215 220

Ile Ser Arg Thr Lys Val His Ser Leu Pro Asn His Gly Leu Glu Asn
225 230 235 240

Leu Lys Lys Leu Arg Ala Arg Ser Thr Tyr Arg Leu Lys Lys Leu Pro
245 250 255

Asn Leu Asp Lys Phe Val Thr Leu Met Glu Ala Ser Leu Thr Tyr Pro
260 265 270

Ser His Cys Cys Ala Phe Ala Asn Leu Lys Arg Gln Ile Ser Glu Leu
275 280 285

His Pro Ile Cys Asn Lys Ser Ile Leu Arg Gln Asp Ile Asp Asp Met
290 295 300

Thr Gln Ile Gly Asp Gln Arg Val Ser Leu Ile Asp Asp Glu Pro Ser
305 310 315 320

Tyr	Gly	Lys	Gly	Ser	Asp	Met	Met	Tyr	Asn	Glu	Phe	Asp	Tyr	Asp	Leu	
						325			330					335		
Cys	Asn	Glu	Val	Val	Asp	Val	Thr	Cys	Ser	Pro	Lys	Pro	Asp	Ala	Phe	
						340			345					350		
Asn	Pro	Cys	Glu	Asp	Ile	Met	Gly	Tyr	Asn	Ile	Leu	Arg	Val	Leu	Ile	
						355			360					365		
Trp	Phe	Ile	Ser	Ile	Leu	Ala	Ile	Thr	Gly	Asn	Thr	Thr	Val	Leu	Val	
						370			375					380		
Val	Leu	Thr	Thr	Ser	Gln	Tyr	Lys	Leu	Thr	Val	Pro	Arg	Phe	Leu	Met	
						385			390					400		
Cys	Asn	Leu	Ala	Phe	Ala	Asp	Leu	Cys	Ile	Gly	Ile	Tyr	Leu	Leu	Leu	
						405			410					415		
Ile	Ala	Ser	Val	Asp	Ile	His	Thr	Lys	Ser	Gln	Tyr	His	Asn	Tyr	Ala	
						420			425					430		
Ile	Asp	Trp	Gln	Thr	Gly	Ala	Gly	Cys	Asp	Ala	Ala	Gly	Phe	Phe	Thr	
						435			440					445		
Val	Phe	Ala	Ser	Glu	Leu	Ser	Val	Tyr	Thr	Leu	Thr	Ala	Ile	Thr	Leu	
						450			455					460		
Glu	Arg	Trp	His	Thr	Ile	Thr	His	Ala	Met	Gln	Leu	Glu	Cys	Lys	Val	
						465			470					480		
Gln	Leu	Arg	His	Ala	Ala	Ser	Val	Met	Val	Leu	Gly	Trp	Thr	Phe	Ala	
						485			490					495		
Phe	Ala	Ala	Ala	Leu	Phe	Pro	Ile	Phe	Gly	Ile	Ser	Ser	Tyr	Met	Lys	
						500			505					510		
Val	Ser	Ile	Cys	Leu	Pro	Met	Asp	Ile	Asp	Ser	Pro	Leu	Ser	Gln	Leu	
						515			520					525		
Tyr	Val	Met	Ala	Leu	Leu	Val	Leu	Asn	Val	Leu	Ala	Phe	Val	Val	Ile	
						530			535					540		
Cys	Gly	Cys	Tyr	Thr	His	Ile	Tyr	Leu	Thr	Val	Arg	Asn	Pro	Thr	Ile	
						545			550					560		
Val	Ser	Ser	Ser	Ser	Asp	Thr	Lys	Ile	Ala	Lys	Arg	Met	Ala	Thr	Leu	
						565			570					575		

Ile Phe Thr Asp Phe Leu Cys Met Ala Pro Ile Ser Phe Phe Ala Ile			
580	585	590	
Ser Ala Ser Leu Lys Val Pro Leu Ile Thr Val Ser Lys Ala Lys Ile			
595	600	605	
Leu Leu Val Leu Phe Tyr Pro Ile Asn Ser Cys Ala Asn Pro Phe Leu			
610	615	620	
Tyr Ala Ile Phe Thr Lys Asn Phe Arg Arg Asp Phe Phe Ile Leu Leu			
625	630	635	640
Ser Lys Phe Gly Cys Tyr Glu Met Gln Ala Gln Ile Tyr Arg Thr Glu			
645	650	655	
Thr Ser Ser Ala Thr His Asn Phe His Ala Arg Lys Ser His Cys Ser			
660	665	670	
Ser Ala Pro Arg Val Thr Asn Ser Tyr Val Leu Val Pro Leu Asn His			
675	680	685	
Ser Ser Gln Asn			
690			
.			
<210> 12			
<211> 688			
<212> PRT			
<213> Rattus norvegicus			
.			
<400> 12			
Met Ala Leu Leu Leu Val Ser Leu Leu Ala Phe Leu Gly Thr Gly Ser			
1	5	10	15
Gly Cys His His Trp Leu Cys His Cys Ser Asn Arg Val Phe Leu Cys			
20	25	30	
Gln Asp Ser Lys Val Thr Glu Ile Pro Thr Asp Leu Pro Arg Asn Ala			
35	40	45	
Ile Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Pro Lys Gly			
50	55	60	
Ser Phe Ala Gly Phe Gly Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn			
65	70	75	80
Asp Val Leu Glu Val Ile Glu Ala Asp Val Phe Ser Asn Leu Pro Lys			
85	90	95	

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asn
100 105 110

Pro Glu Ala Phe Gln Asn Leu Pro Ser Leu Arg Tyr Leu Leu Ile Ser
115 120 125

Asn Thr Gly Ile Lys His Leu Pro Ala Val His Lys Ile Gln Ser Leu
130 135 140

Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Ile Val
145 150 155 160

Ala Arg Asn Ser Phe Met Gly Leu Ser Phe Glu Trp Leu Ser Lys Asn
165 170 175

Gly Ile Glu Glu Ile His Asn Cys Ala Phe Asn Gly Thr Gln Leu Asp
180 185 190

Glu Leu Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu Leu Pro Asn Asp
195 200 205

Val Phe Gln Gly Ala Ser Gly Pro Val Ile Leu Asp Ile Ser Arg Thr
210 215 220

Lys Val His Ser Leu Pro Asn His Gly Leu Glu Asn Leu Lys Lys Leu
225 230 235 240

Arg Ala Arg Ser Thr Tyr Arg Trp Lys Lys Leu Pro Asn Leu Asp Lys
245 250 255

Phe Val Thr Leu Met Glu Ala Ser Leu Thr Tyr Pro Ser His Cys Cys
260 265 270

Ala Phe Ala Asn Leu Lys Arg Gln Ile Ser Glu Leu His Pro Ile Cys
275 280 285

Asn Lys Ser Ile Leu Arg Gln Asp Ile Asp Asp Met Thr Gln Ile Gly
290 295 300

Asp Gln Arg Val Ser Leu Ile Asp Asp Glu Pro Ser Tyr Gly Lys Gly
305 310 315 320

Ser Asp Met Met Tyr Asn Glu Phe Asp Tyr Asp Leu Cys Asn Glu Val
325 330 335

Val Asp Val Thr Cys Ser Pro Lys Pro Asp Ala Phe Asn Pro Cys Glu
340 345 350

Asp Ile Met Gly Tyr Asn Ile Leu Arg Val Leu Ile Trp Phe Ile Ser
355 360 365

Ile Leu Ala Ile Thr Gly Asn Thr Thr Val Leu Val Val Leu Thr Thr
370 375 380

Ser Gln Tyr Lys Leu Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ala
385 390 395 400

Phe Ala Asp Leu Cys Ile Gly Ile Tyr Leu Leu Ile Ala Ser Val
405 410 415

Asp Ile His Thr Lys Ser Gln Tyr His Asn Tyr Ala Ile Asp Trp Gln
420 425 430

Thr Gly Ala Gly Cys Asp Ala Ala Gly Phe Phe Thr Val Phe Ala Ser
435 440 445

Glu Leu Ser Val Tyr Thr Leu Thr Ala Ile Thr Leu Glu Arg Trp His
450 455 460

Thr Ile Thr His Ala Met Gln Leu Glu Cys Lys Val Gln Leu Arg His
465 470 475 480

Ala Ala Ser Val Met Val Leu Gly Trp Thr Phe Ala Phe Ala Ala Ala
485 490 495

Leu Phe Pro Ile Phe Gly Ile Ser Ser Tyr Met Lys Val Ser Ile Cys
500 505 510

Leu Pro Met Asp Ile Asp Ser Pro Leu Ser Gln Leu Tyr Val Met Ala
515 520 525

Leu Leu Val Leu Asn Val Leu Ala Phe Val Val Ile Cys Gly Cys Tyr
530 535 540

Thr His Ile Tyr Leu Thr Val Arg Asn Pro Thr Ile Val Ser Ser Ser
545 550 555 560

Ser Asp Thr Lys Ile Ala Lys Arg Met Ala Thr Leu Ile Phe Thr Asp
565 570 575

Phe Leu Cys Met Ala Pro Ile Ser Phe Phe Ala Ile Ser Ala Ser Leu
580 585 590

Lys Val Pro Leu Ile Thr Val Ser Lys Ala Lys Ile Leu Leu Val Leu
595 600 605

Phe Tyr Pro Ile Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe
610 615 620

Thr Lys Asn Phe Arg Arg Asp Phe Phe Ile Leu Leu Ser Lys Phe Gly
625 630 635 640

Cys Tyr Glu Met Gln Ala Gln Ile Tyr Arg Thr Glu Thr Ser Ser Ala
645 650 655

Thr His Asn Phe His Ala Arg Lys Ser His Cys Ser Ser Ala Pro Arg
660 665 670

Val Thr Asn Ser Tyr Val Leu Val Pro Leu Asn His Ser Ser Gln Asn
675 680 685

<210> 13
<211> 687
<212> PRT
<213> Equus asinus

<400> 13
Met Ala Leu Leu Leu Val Ser Leu Leu Ala Phe Leu Ser Leu Gly Ser
1 5 10 15

Gly Cys His His Gln Val Cys His Tyr Ser Asn Arg Val Phe Leu Cys
20 25 30

Gln Glu Ser Lys Val Thr Glu Ile Pro Ser Asp Leu Pro Arg Asn Ala
35 40 45

Leu Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Pro Lys Gly
50 55 60

Ala Phe Ser Gly Phe Gly Asp Leu Lys Lys Ile Glu Ile Ser Gln Asn
65 70 75 80

Asp Val Leu Glu Val Ile Glu Ala Asn Val Phe Ser Asn Leu Pro Lys
85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asp
100 105 110

His Asp Ala Phe Gln Asn Leu Pro Asn Leu Gln Tyr Leu Leu Ile Ser

115	120	125
Asn Thr Gly Ile Lys His Leu Pro Ala Val His Lys Ile Gln Ser Leu		
130	135	140
Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Ile Val		
145	150	155
160		
Glu Arg Asn Ser Phe Met Gly Leu Ser Phe Glu Ser Met Ile Leu Arg		
165	170	175
Leu Ser Lys Asn Gly Ile Gln Glu Ile His Asn Cys Ala Phe Asn Gly		
180	185	190
Thr Gln Leu Asp Glu Leu Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu		
195	200	205
Leu Pro Asn Asp Val Phe Gln Gly Ala Ser Gly Pro Val Ile Leu Asp		
210	215	220
Ile Ser Gly Thr Arg Ile His Ser Leu Pro Asn Tyr Gly Leu Glu Asn		
225	230	235
240		
Leu Lys Lys Leu Arg Ala Arg Ser Thr Tyr Asn Leu Lys Lys Leu Pro		
245	250	255
Ser Leu Glu Lys Phe Val Ala Leu Met Glu Ala Ser Leu Thr Tyr Pro		
260	265	270
Ser His Cys Cys Ala Phe Ala Asn Trp Arg Gln Gln Thr Ser Glu Leu		
275	280	285
Gln Thr Thr Cys Asn Lys Ser Ile Leu Arg Gln Glu Val Asp Met Thr		
290	295	300
Gln Ala Arg Gly Glu Arg Val Ser Leu Ala Glu Asp Asp Glu Ser Met		
305	310	315
320		
Met Tyr Ser Glu Phe Asp Tyr Asp Leu Cys Asn Glu Val Val Asp Val		
325	330	335
Thr Cys Ser Pro Lys Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met		
340	345	350
Gly Tyr Asp Ile Leu Arg Val Leu Ile Trp Phe Ile Ser Ile Leu Ala		
355	360	365
Ile Thr Gly Asn Ile Ile Val Leu Val Ile Leu Ile Thr Ser Gln Tyr		

370	375	380
Lys Leu Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp		
385	390	395
Leu Cys Ile Gly Ile Tyr Leu Leu Leu Ile Ala Ser Val Asp Ile His		
405	410	415
Thr Lys Ser Gln Tyr His Asn Tyr Ala Ile Asp Trp Gln Thr Gly Ala		
420	425	430
Gly Cys Asp Ala Ala Gly Phe Phe Thr Val Phe Gly Ser Glu Leu Ser		
435	440	445
Val Tyr Thr Leu Thr Ala Ile Thr Leu Glu Arg Trp His Thr Ile Thr		
450	455	460
His Ala Met Gln Leu Glu Cys Lys Val Gln Leu Arg His Ala Ala Ser		
465	470	475
Val Met Leu Val Gly Trp Ile Phe Gly Phe Gly Val Gly Leu Leu Pro		
485	490	495
Ile Phe Gly Ile Ser Thr Tyr Met Lys Val Ser Ile Cys Leu Pro Met		
500	505	510
Asp Ile Asp Ser Pro Leu Ser Gln Leu Tyr Val Met Ser Leu Leu Val		
515	520	525
Leu Asn Val Leu Ala Phe Val Val Ile Cys Gly Cys Tyr Thr His Ile		
530	535	540
Tyr Leu Thr Val Arg Asn Pro Asn Ile Val Ser Ser Ser Asp Thr		
545	550	555
Lys Ile Ala Lys Arg Met Gly Ile Leu Ile Phe Thr Asp Phe Leu Cys		
565	570	575
Met Ala Pro Ile Ser Phe Phe Gly Ile Ser Ala Ser Leu Lys Val Ala		
580	585	590
Leu Ile Thr Val Ser Lys Ser Lys Ile Leu Leu Val Leu Phe Tyr Pro		
595	600	605
Ile Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Asn		
610	615	620
Phe Arg Arg Asp Phe Phe Ile Leu Leu Ser Lys Phe Gly Cys Tyr Glu		

625 630 635 640

Met Gln Ala Gln Thr Tyr Arg Thr Glu Thr Ser Ser Thr Gly His Ile
645 650 655

Ser His Pro Lys Asn Gly Pro Cys Pro Pro Thr Pro Arg Val Thr Asn
660 665 670

Gly Ala Asn Cys Thr Leu Val Pro Leu Ser His Leu Ala Gln Asn
675 680 685

<210> 14

<211> 693

<212> PRT

<213> CHICKEN

<400> 14

Met Ser Leu Gly Leu Thr Cys Leu Leu Ile Leu Leu Ala Ser Cys Ser
1 5 10 15

Gly Cys Gln His His Thr Cys Leu Cys Glu Gly Arg Ile Phe Ile Cys
20 25 30

Gln Glu Ile Lys Val Val Gln Leu Pro Arg Asp Ile Pro Thr Asn Ala
35 40 45

Thr Glu Leu Arg Phe Val Leu Thr Lys Met Arg Val Ile Pro Lys Gly
50 55 60

Ala Phe Thr Gly Leu His Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn
65 70 75 80

Asp Ala Leu Glu Ile Ile Glu Gly Asn Val Phe Ser Ser Leu Pro Lys
85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Lys Leu Met Lys Ile Asp
100 105 110

Gln Asp Ala Phe Gln His Leu Pro Ser Leu Arg Tyr Leu Leu Ile Ser
115 120 125

Asn Thr Gly Leu Ser Phe Leu Pro Val Val His Lys Val His Ser Phe
130 135 140

Gln Lys Val Leu Leu Asp Val Gln Asp Asn Ile His Ile Arg Thr Ile
145 150 155 160

Glu Arg Asn Thr Phe Met Gly Leu Ser Ser Glu Ser Val Ile Leu Arg
165 170 175

Leu Asn Lys Asn Gly Ile Gln Glu Ile Lys Asp His Ala Phe Asn Gly
180 185 190

Thr Cys Leu Asp Glu Leu Asn Leu Ser Asp Asn Tyr Asn Leu Glu Lys
195 200 205

Leu Pro Glu Lys Val Phe Gln Gly Ala Ile Gly Pro Val Val Leu Asp
210 215 220

Ile Ser Arg Thr Arg Ile Ser Phe Leu Pro Ser His Gly Leu Glu Phe
225 230 235 240

Ile Lys Lys Leu Arg Ala Arg Ser Thr Tyr Lys Leu Lys Lys Leu Pro
245 250 255

Asp Val Asn Lys Phe Arg Ser Leu Ile Glu Ala Asn Phe Thr Tyr Pro
260 265 270

Ser His Cys Cys Ala Phe Thr Asn Arg Lys Thr Gln Asn Thr Glu Phe
275 280 285

Tyr Pro Ile Cys Ser Met Ser Pro Ala Lys Gln Asp Leu Gly Glu Gln
290 295 300

Thr Gly Lys Arg Lys His Arg Arg Ser Ala Ala Glu Asp Tyr Ile Ser
305 310 315 320

His Tyr Gly Thr Arg Phe Gly Pro Val Glu Asn Glu Phe Asp Tyr Gly
325 330 335

Leu Cys Asn Glu Val Val Asp Phe Val Cys Ser Pro Lys Pro Asp Ala
340 345 350

Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Asn Val Leu Arg Val Leu
355 360 365

Ile Trp Phe Ile Asn Ile Leu Ala Ile Thr Gly Asn Thr Thr Val Leu
370 375 380

Ile Ile Leu Ile Ser Ser Gln Tyr Lys Leu Thr Val Pro Arg Phe Leu
385 390 395 400

Met Cys Asn Leu Ala Phe Ala Asp Leu Cys Ile Gly Ile Tyr Leu Leu
405 410 415

Phe Ile Ala Ser Val Asp Ile Gln Thr Lys Ser Arg Tyr Tyr Asn Tyr
420 425 430

Ala Ile Asp Trp Gln Thr Gly Ala Gly Cys Asn Ala Ala Gly Phe Phe
435 440 445

Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu Thr Val Ile Thr
450 455 460

Leu Glu Arg Trp His Thr Ile Thr Tyr Ala Met Gln Leu Asn Arg Lys
465 470 475 480

Val Arg Leu Arg His Ala Val Ile Ile Met Val Phe Gly Trp Met Phe
485 490 495

Ala Phe Thr Val Ala Leu Leu Pro Ile Phe Gly Ile Ser Ser Tyr Met
500 505 510

Lys Val Ser Ile Cys Leu Pro Met His Ile Glu Thr Pro Phe Ser Gln
515 520 525

Ala Tyr Val Ile Phe Leu Leu Val Leu Asn Val Leu Ala Phe Val Ile
530 535 540

Ile Cys Ile Cys Tyr Ile Cys Ile Tyr Phe Thr Val Arg Asn Pro Asn
545 550 555 560

Val Ile Ser Ser Asn Ser Asp Thr Lys Ile Ala Lys Arg Met Ala Ile
565 570 575

Leu Ile Phe Thr Asp Phe Leu Cys Met Ala Pro Ile Ser Phe Phe Ala
580 585 590

Ile Ser Ala Ser Leu Arg Val Pro Leu Ile Thr Val Ser Lys Ser Lys
595 600 605

Ile Leu Leu Val Leu Phe Tyr Pro Ile Asn Ser Cys Ala Asn Pro Phe
610 615 620

Leu Tyr Ala Ile Phe Thr Lys Thr Phe Arg Arg Asp Phe Phe Ile Leu
625 630 635 640

Leu Ser Lys Phe Gly Cys Cys Glu Met Gln Ala Gln Ile Tyr Arg Thr
645 650 655

Glu Thr Ser Ser Ser Ala His Asn Phe His Thr Arg Asn Gly His Tyr
660 665 670

Pro Thr Ala Ser Lys Asn Ser Asp Gly Thr Ile Tyr Ser Leu Val Pro
675 680 685

Leu Asn His Leu Asn
690

<210> 15
<211> 676
<212> PRT
<213> Callithrix jacchus

<400> 15
Met Lys Gln Pro Leu Leu Ala Leu Gln Leu Leu Lys Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Pro Leu Pro Pro Leu Pro Arg Ala Leu Arg Glu Ala Arg
20 25 30

Cys Cys Pro Glu Pro Cys Asn Cys Thr Pro Asp Gly Ala Leu Arg Cys
 35 40 45

Pro Gly Pro Gly Ala Gly Leu Thr Arg Leu Ser Leu Ala Tyr Leu Pro
50 55 60

Val Lys Val Ile Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val Ile
65 70 75 80

Lys Ile Glu Ile Ser Gln Ser Asp Ser Leu Glu Arg Ile Glu Ala Asn
85 90 95

Ala Phe Asp Asn Leu Leu Asn Leu Ser Glu Ile Leu Ile Gln Asn Thr
 100 105 110

Lys Asn Leu Ile His Ile Glu Pro Gly Ala Phe Thr Asn Leu Pro Arg
115 120 125

Leu Lys Tyr Leu Ser Ile Cys Asn Thr Gly Ile Arg Lys Phe Pro Asp
130 135 140

Val Thr Lys Ile Phe Ser Ser Glu Thr Asn Phe Ile Leu Glu Ile Cys
 145 150 155 160

Asp Asn Leu His Ile Thr Thr Ile Pro Gly Asn Ala Phe Gln Gly Met
165 170 175

Asn Asn Glu Ser Ile Thr Leu Lys Leu Tyr Gly Asn Gly Phe Glu Glu
 180 185 186

Val Gln Ser His Ala Phe Asn Gly Thr Thr Val Ile Ser Leu Val Leu
195 200 205

Lys Glu Asn Val His Leu Glu Arg Ile His Asn Gly Ala Phe Arg Gly
210 215 220

Ala Thr Gly Pro Ser Ile Leu Asp Ile Ser Ser Thr Lys Leu Gln Ala
225 230 235 240

Leu Pro Ser His Gly Leu Glu Ser Ile Gln Thr Leu Ile Ala Thr Ser
245 250 255

Ser Tyr Ser Leu Lys Lys Leu Pro Ser Arg Glu Lys Phe Ala Asn Leu
260 265 270

Leu Asp Ala Thr Leu Thr Tyr Pro Ser His Cys Cys Ala Phe Arg Asn
275 280 285

Val Pro Thr Lys Asp Tyr Pro Ala Ile Phe Ala Glu Ser Gly Gln Ser
290 295 300

Gly Trp Asp Tyr Asp Tyr Gly Phe His Leu Pro Lys Thr Pro Arg Cys
305 310 315 320

Ala Pro Glu Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr
325 330 335

Asp Phe Leu Arg Val Leu Ile Trp Leu Ile Asn Ile Leu Ala Ile Met
340 345 350

Gly Asn Met Thr Val Leu Phe Val Leu Leu Thr Ser Arg Tyr Lys Leu
355 360 365

Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ser Phe Ala Asp Phe Cys
370 375 380

Met Gly Leu Tyr Leu Leu Ile Ala Ser Val Asp Ser Gln Thr Lys
385 390 395 400

Gly Gln Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Ser Gly Cys
405 410 415

Asn Thr Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr
420 425 430

Thr Leu Thr Val Ile Thr Leu Glu Arg Trp His Thr Ile Thr Tyr Ala
435 440 445

Ile His Leu Asp Gln Lys Leu Arg Leu Arg His Ala Ile Leu Ile Met
450 455 460

Leu Gly Gly Trp Leu Phe Ser Ser Leu Ile Ala Met Leu Pro Leu Val
465 470 475 480

Gly Val Ser Asn Tyr Met Lys Val Ser Ile Cys Leu Pro Met His Ile
485 490 495

Glu Thr Pro Phe Ser Gln Ala Tyr Val Ile Phe Leu Leu Val Leu Asn
500 505 510

Val Leu Ala Phe Val Ile Ile Cys Ile Cys Tyr Ile Cys Ile Tyr Phe
515 520 525

Thr Val Arg Asn Pro Asn Val Ile Ser Ser Asn Ser Asp Thr Lys Ile
530 535 540

Ala Lys Lys Met Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys Met Ala
545 550 555 560

Pro Ile Ser Phe Phe Ala Ile Ser Ala Ala Phe Lys Met Pro Leu Ile
565 570 575

Thr Val Thr Asn Ser Lys Val Leu Leu Val Leu Phe Tyr Pro Ile Asn
580 585 590

Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Thr Phe Arg
595 600 605

Arg Asp Phe Phe Leu Leu Leu Gly Lys Phe Gly Cys Cys Lys His Arg
610 615 620

Ala Glu Leu Tyr Arg Arg Lys Asp Phe Ser Ala Tyr Thr Ser Asn Tyr
625 630 635 640

Lys Asn Gly Phe Thr Gly Ser Ser Lys Pro Ser Gln Ser Thr Leu Lys
645 650 655

Leu Pro Ala Leu His Cys Gln Gly Thr Ala Leu Leu Asp Lys Thr Cys
660 665 670

Tyr Lys Glu Tyr
675

<211> 907

<212> PRT

<213> HUMAN

<400> 16

Met Asp Thr Ser Arg Leu Gly Val Leu Leu Ser Leu Pro Val Leu Leu
1 5 10 15

Gln Leu Ala Thr Gly Gly Ser Ser Pro Arg Ser Gly Val Leu Leu Arg
20 25 30

Gly Cys Pro Thr His Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu
35 40 45

Arg Val Asp Cys Ser Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu
50 55 60

Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln
65 70 75 80

Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg
85 90 95

Leu Ala Gly Asn Ala Leu Thr Tyr Ile Pro Lys Gly Ala Phe Thr Gly
100 105 110

Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg His
115 120 125

Val Pro Thr Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg
130 135 140

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
145 150 155 160

Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu
165 170 175

Ile Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr
180 185 190

Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn
195 200 205

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser
210 215 220

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp

225

230

235

240

Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu
245 250 255

Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
260 265 270

Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
275 280 285

Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu
290 295 300

Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu
305 310 315 320

Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr
325 330 335

Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro
340 345 350

Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro
355 360 365

Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
370 375 380

Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu
385 390 395 400

Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn
405 410 415

Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn
420 425 430

Leu Leu Ser Ser Phe Pro Ile Thr Gly Leu His Gly Leu Thr His Leu
435 440 445

Lys Leu Thr Gly Asn His Ala Leu Gln Ser Leu Ile Ser Ser Glu Asn
450 455 460

Phe Pro Glu Leu Lys Val Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys
465 470 475 480

Ala Phe Gly Val Cys Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn

485

490

495

Lys Gly Asp Asn Ser Ser Met Asp Asp Leu His Lys Lys Asp Ala Gly
 500 505 510

Met Phe Gln Ala Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp
 515 520 525

Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser
 530 535 540

Pro Gly Pro Phe Lys Pro Cys Glu His Leu Leu Asp Gly Trp Leu Ile
 545 550 555 560

Arg Ile Gly Val Trp Thr Ile Ala Val Leu Ala Leu Thr Cys Asn Ala
 565 570 575

Leu Val Thr Ser Thr Val Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile
 580 585 590

Lys Leu Leu Ile Gly Val Ile Ala Ala Val Asn Met Leu Thr Gly Val
 595 600 605

Ser Ser Ala Val Leu Ala Gly Val Asp Ala Phe Thr Phe Gly Ser Phe
 610 615 620

Ala Arg His Gly Ala Trp Trp Glu Asn Gly Val Gly Cys His Val Ile
 625 630 635 640

Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr
 645 650 655

Leu Ala Ala Leu Glu Arg Gly Phe Ser Val Lys Tyr Ser Ala Lys Phe
 660 665 670

Glu Thr Lys Ala Pro Phe Ser Ser Leu Lys Val Ile Ile Leu Leu Cys
 675 680 685

Ala Leu Leu Ala Leu Thr Met Ala Ala Val Pro Leu Leu Gly Gly Ser
 690 695 700

Lys Tyr Gly Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro
 705 710 715 720

Ser Thr Met Gly Tyr Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys
 725 730 735

Phe Leu Met Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp

740

745

750

Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Val Lys His Ile
755 760 765

Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Asn Cys Pro Val Ala Phe
770 775 780

Leu Ser Phe Ser Ser Leu Ile Asn Leu Thr Phe Ile Ser Pro Glu Val
785 790 795 800

Ile Lys Phe Ile Leu Leu Val Val Val Pro Leu Pro Ala Cys Leu Asn
805 810 815

Pro Leu Leu Tyr Ile Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val
820 825 830

Ser Leu Arg Lys Gln Thr Tyr Val Trp Thr Arg Ser Lys His Pro Ser
835 840 845

Leu Met Ser Ile Asn Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser
850 855 860

Thr Gln Ala Leu Val Thr Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu
865 870 875 880

Pro Pro Ser Ser Val Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys
885 890 895

His Leu Ser Ser Val Ala Phe Val Pro Cys Leu
900 905

<210> 17

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized peptide

<400> 17

Arg Ser Phe Ile Lys Ala Glu Asn Thr Thr His Ala Met Ser Ile Lys
1 5 10 15

<210> 18

<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized peptide

<400> 18
Asp Ile Lys Tyr Arg Gly Gln Tyr Gln Lys Tyr Ala Leu Leu Trp Met
1 5 10 15

Glu Ser Val Gln Cys Arg
20

<210> 19
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized peptide

<400> 19
Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser Asn Ile Arg Pro Gly
1 5 10 15

Lys Arg Gln Thr Ser
20

<210> 20
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized peptide

<400> 20
Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe
1 5 10 15

Pro Leu Tyr Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser
20 25 30

<210> 21
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized peptide

<400> 21
Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr Glu Val Arg Asn Cys Phe
1 5 10 15

Gly Arg Glu Val Ala Val Ala Asn Arg
20 25

<210> 22
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized peptide

<400> 22
Arg Val Glu Ile Pro Asp Thr Met Thr Ser Trp
1 5 10

<210> 23
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized peptide

<400> 23
Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln Leu Leu His Lys His Gln
1 5 10 15

Arg Lys Ser Ile Phe Lys Ile Lys Lys Ser Leu Ser Thr Ser Ile
20 25 30

Val Trp Ile Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu Asn Lys
35 40 45

Ile Thr Leu Gly Asp Ser Ile Met Lys Pro Val Ser
50 55 60

<210> 24

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GPCR21-F1
forward primer

<400> 24

tgtgttaagg ccacgctgtt ag 22

<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GPCR21-R1
reverse primer

<400> 25

tcactgtat ggcaaggatg a 21

<210> 26

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-F3
forward primer

<400> 26

agcccgagcca catcgct 17

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<210> 27
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GAPDH-R1
      reverse primer

<400> 27
gtgaccaggc gcccaatac                                19

<210> 28
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GAPDH-PVIC
      Taqman(R) Probe

<400> 28
caaatccgtt gactccgacc ttcacacct                                28

<210> 29
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide 1

<220>
<221> modified_base
<222> (25)..(84)
<223> n=a or g or c or t; k=c or g or t

<400> 29
cgaagcgtaa gggcccagcc ggccnnknnk nnknnknnkn nknnknnknn knnknnknnk 60
nnknnknnkn nknnknnkn knnkccgggt ccgggcggc                                99

<210> 30

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<211> 95
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<220>
<223> Description of Artificial Sequence:
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<220>
<221> modified_base
<222> (21)..(80)
<223> n=a or g or c or t; v=c or a or g

<400> 30
aaaaggaaaa aagcgccgc vnnvnnvnnv nnvnnvnnvn nvnnvnnvnn vnnvnnvnnv 60
nnvnnvnnvn nvnnvnnvnn gccggccgga cccgg 95

<210> 31
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 31
Pro Gly Pro Gly Gly
1 5

<210> 32
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 32
Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys Ile His
1 5 10

<210> 33
<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 33

Cys Ile Arg His Ile Ser Arg Lys Ala Phe Phe Gly Leu
1 5 10

<210> 34

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 34

His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys
1 5 10

<210> 35

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 35

Pro Ile Thr Arg Ile Ser Gln Arg Leu Phe Thr Gly Leu
1 5 10

<210> 36

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 36

Glu Lys Thr Phe Ser Ser Leu Lys Asn Leu Gly Glu Leu
1 5 10

<210> 37

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 37

Lys Asn Gln Phe Glu Ser Leu Lys Gln Leu Gln Ser Leu
1 5 10

<210> 38

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 38

Thr Thr His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala
1 5 10

<210> 39

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 39

Ile Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu Asn
1 5 10

<210> 40
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 40
Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp
1 5 10

<210> 41
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 41
Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys
1 5 10

<210> 42
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 42
Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu
1 5 10

<210> 43
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 43

Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn
1 5 10

<210> 44

<211> 14

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 44

Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn
1 5 10

<210> 45

<211> 14

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 45

Val Leu Asn Lys Ile Thr Leu Gly Asp Ser Ile Met Lys Pro
1 5 10

<210> 46

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 46

Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile
1 5 10

<210> 47
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 47
Ser Ile Phe Lys Ile Lys Lys Ser Leu Ser Thr Ser Ile
1 5 10

<210> 48
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 48
Tyr Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala
1 5 10

<210> 49
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 49
Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys Lys
1 5 10

<210> 50
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 50

Ile Lys Tyr Leu Thr Asn Ser Thr Phe Leu Ser Cys Asp Ser
1 5 10

<210> 51

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 51

Leu Leu Gln Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr
1 5 10

<210> 52

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 52

Pro Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe Lys Asn
1 5 10

<210> 53

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 53

Phe Ile Lys Ala Glu Asn Thr Thr His Ala Met Ser Ile Lys
1 5 10

<210> 54
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 54
Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala Asn Ser Val Ala
1 5 10 15

<210> 55
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 55
Phe Gly Thr Val His Gly Asn Ala Asn Ser Val Ala Leu Thr Gln Glu
1 5 10 15

<210> 56
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 56
Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe
1 5 10 15

<210> 57
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 57
Ile Gly Tyr Ser Leu Gly Ile Phe Leu Gly Val Asn Leu Leu Ala Phe
1 5 10 15

<210> 58
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 5' primer

<400> 58
gcagcagcgg ccgcagaata tttgtctggg ttatagc 37

<210> 59
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 3' primer

<400> 59
gcagcagtcg acggaaactg gtttcattat actgtc 36

<210> 60
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 5' primer

<400> 60

gcagcagcg ccgcatgttc tttctacttc atttcatcg

39

<210> 61

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 3'
primer

<400> 61

gcagcagtgc acgggtgtga gagtatagag cattgg

36